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<p>(54) Title: DIABETES THERAPY</p> <p>(57) Abstract</p> <p>The invention provides a gene therapy method for delivering safe and effective, long-term amounts of GLP-1(7-37)-based proteins useful for treating Type I and Type II diabetes. The invention eliminates the need for subcutaneous injections and is able to provide tight glucose control.</p>		

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DIABETES THERAPY

The present invention relates to gene therapy and provides stable, transformed mammalian cell lines and vectors useful as vehicles for transferring functional DNA sequences
5 whose protein products are useful in the treatment of *diabetes mellitus*.

The human hormone glucagon is a 29-amino acid hormone produced in pancreatic A-cells. The hormone belongs to a multi-gene family of structurally related peptides that
10 include secretin, gastric inhibitory peptide, vasoactive intestinal peptide and glicentin. These peptides variously regulate carbohydrate metabolism, gastrointestinal mobility and secretory processing. However, the principal recognized actions of pancreatic glucagon are to promote hepatic
15 glycogenolysis and gluconeogenesis, resulting in an elevation of blood sugar levels. In this regard, the actions of glucagon are counter regulatory to those of insulin and may contribute to the hyperglycemia that accompanies *diabetes mellitus* (Lund, P.K., et al., *Proc. Natl. Acad. Sci. U.S.A.*,
20 79:345-349 (1982)).

When glucagon binds to its receptor on insulin producing cells, cAMP production increases which in turn stimulates insulin expression (Korman, L.Y., et al., *Diabetes*, 34:717-722 (1985)). Moreover, high levels of
25 insulin down-regulate glucagon synthesis by a feedback inhibition mechanism (Ganong, W.F., *Review of Medical Physiology*, Lange Publications, Los Altos, California, p. 273 (1979)). Thus, the expression of glucagon is carefully regulated by insulin, and ultimately by serum glucose levels.

30 Preproglucagon, the precursor form of glucagon, is encoded by a 360 base pair gene and is processed to form proglucagon (Lund, et al., *Proc. Natl. Acad. Sci. U.S.A.* 79:345-349 (1982)). Patzelt, et al. (*Nature*, 282:260-266 (1979)) demonstrated that proglucagon is further processed
35 into glucagon and a second peptide. Later experiments demonstrated that proglucagon is cleaved carboxyl to Lys-Arg

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or Arg-Arg residues (Lund, P.K., et al., Lopez L.C., et al., *Proc. Natl. Acad. Sci. U.S.A.*, 80:5485-5489 (1983), and Bell, G.I., et al., *Nature* 302:716-718 (1983)). Bell, G.I., et al., also discovered that proglucagon contained three
5 discrete and highly homologous peptide regions which were designated glucagon, glucagon-like peptide 1 (GLP-1), and glucagon-like peptide 2 (GLP-2). Lopez, et al., demonstrated that GLP-1 was a 37 amino acid peptide and that GLP-2 was a
10 34 amino acid peptide. Analogous studies on the structure of rat preproglucagon revealed a similar pattern of proteolytic cleavage at Lys-Arg or Arg-Arg residues, resulting in the formation of glucagon, GLP-1, and GLP-2 (Heinrich, G., et al., *Endocrinol.*, 115:2176-2181 (1984)). Finally, human,
15 rat, bovine, and hamster sequences of GLP-1 have been found to be identical (Ghiglione, M., et al., *Diabetologia*, 27:599-600 (1984)).

The conclusion reached by Lopez, et al., regarding the size of GLP-1 was confirmed by studying the molecular forms of GLP-1 found in the human pancreas (Uttenthal, L.O.,
20 et al. *J. Clin. Endocrinol. Metabol.*, 61:472-479 (1985)). Their research showed that GLP-1 and GLP-2 are present in the pancreas as 37 and 34 amino acid peptides respectively.

The similarity between GLP-1 and glucagon suggested to early investigators that GLP-1 might have biological
25 activity. Although some investigators found that GLP-1 could induce rat brain cells to synthesize cAMP (Hoosein, N.M., et al., *Febs Lett.* 178:83-86 (1984)), other investigators failed to identify any physiological role for GLP-1 (Lopez, L.C., et al. *supra*). The failure to identify any physiological role
30 for GLP-1 caused some investigators to question whether GLP-1 was in fact a hormone and whether the relatedness between glucagon and GLP-1 might be artifactual.

It has now been shown that biologically processed forms of GLP-1 have insulinotropic properties and delay
35 gastric emptying. GLP-1(7-34) and GLP-1(7-35) are disclosed in U.S. Patent No: 5,118,666, herein incorporated by

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reference. GLP-1(7-37) is disclosed in U.S. Patent No: 5,120,712, herein incorporated by reference.

Variants and analogs of GLP-1 are known in the art. These variants and analogs include, for example, GLP-1(7-36),
5 Gln⁹-GLP-1(7-37), Thr¹⁶-Lys¹⁸-GLP-1(7-37), and Lys¹⁸-GLP-1(7-37). Derivatives of GLP-1 include, for example, acid addition salts, carboxylate salts, lower alkyl esters, and amides (see, e.g., WO91/11457). Generally, the various disclosed forms of GLP-1 are known to stimulate insulin
10 secretion (insulinotropic action) and cAMP formation (see, e.g., Mojsov, S., *Int. J. Peptide Protein Research*, 40:333-343 (1992)).

More importantly, numerous investigators have demonstrated a predictable relationship between various *in*
15 *vitro* laboratory experiments and mammalian, especially human, insulinotropic responses to exogenous administration of GLP-1, GLP-1(7-36) amide, and GLP-1(7-37) acid (see, e.g., Nauck, M.A., et al., *Diabetologia*, 36:741-744 (1993); Gutniak, M., et al., *New England J. of Medicine*, 326(20):1316-1322 (1992);
20 Nauck, M.A., et al., *J. Clin. Invest.*, 91:301-307 (1993); and Thorens, B., et al., *Diabetes*, 42:1219-1225 (1993)).

The fundamental defects responsible for causing hyperglycemia in mature onset diabetes include impaired secretion of endogenous insulin and resistance to the effects
25 of insulin by muscle and liver tissue (Galloway, J.S., *Diabetes Care*, 13:1209-1239, (1990)). The latter defect results in excess glucose production in the liver. Thus, whereas a normal individual releases glucose at the rate of approximately 2 mg/kg/minute, a patient with mature onset
30 diabetes releases glucose at a rate exceeding 2.5 mg/kg/minute, resulting in a net excess of at least 70 grams of glucose per 24 hours.

Because there exists exceedingly high correlation between hepatic glucose production, fasting blood glucose
35 levels, and overall metabolic control as indicated by glycohemoglobin measurements (Galloway, J.A., *supra*; and Galloway, J.A., et al., *Clin. Therap.*, 12:460-472 (1990)), it

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is readily apparent that control of fasting blood glucose is essential for achieving overall normalization of metabolism sufficient to prevent hyperglycemic complications. Since existing insulin therapies rarely normalize hepatic glucose production without producing significant hyperinsulinemia and hypoglycemia (Galloway, J.A., and Galloway, J.A., et al., *supra*) alternative approaches for diabetic therapy are needed.

Therapy based on administration of longer acting GLP-1 analogs is one such approach. To date however, this approach has failed to deliver long term efficacious doses to individuals due in large part because the serum half-life of GLP-1(7-37) is quite short. Therefore, the quest for alternative approaches continues.

Gene therapy offers a new avenue for treating diseases rooted in hormone deficiencies because it operates as an *in vivo* protein production and delivery system. This is an especially attractive approach since gene therapy also offers the possibility of physiologically regulating the production and secretion of proteins in response to homeostatic mediators within the body.

Gene therapy can be effected in a number of ways. Retroviral-mediated gene transfer was suggested for treating human diseases involving malfunctioning bone marrow. Anderson et al., *Science* 226: 401 (1984). In addition, PCT Publication Number WO93/09222 (May 13, 1993) and U.S. Patent Number 5,399,346 (March 21, 1995) disclose the genetic alteration of primary human cells that are cultured then reintroduced into the body for the treatment of a variety of diseases.

Many heritable diseases such as diabetes result from the absence of a functional gene necessary to provide the animal with an adequate supply of a vital protein. The goal of gene therapy is to deliver a nucleic acid sequence, present on an RNA or DNA vector, which is capable of encoding the desired, therapeutic protein. Although a number of methods exist to deliver the DNA or RNA vector containing the

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desired nucleic acid sequence into the target mammalian cells, two procedures termed *ex vivo* and *in vivo* are generally employed.

Ex vivo gene therapy consists of four primary steps: (1) Primary cells (target cells) are removed from the individual in need of therapy; (2) The gene therapy nucleotide sequence is incorporated into the target cell *in vitro*; (3) The transformed cells expressing the incorporated nucleotide sequence encoding the protein of interest are identified, isolated, and expanded; and (4) The transformed cells are reintroduced into the individual.

Ex vivo therapy generally results in the incorporation of the nucleotide sequence encoding the protein of interest into the chromosomal DNA of the target cell. The critical step of *ex vivo* gene therapy is the proper introduction of the nucleotide sequence encoding the desired protein into the target cell. This transfer of DNA can be accomplished by a number of well documented methods such as: calcium phosphate precipitation, electroporation, and adenoviral or retroviral vectors (Current Protocols in Molecular Biology, John Wiley and Sons, 1989; Methods of Cell Biology, 43: 161 - 189, 1994; *Proc. Natl. Acad. Sci. USA* 85: 6460 - 6464, 1988); although, other well known methods are also consistent with this invention.

In vivo gene therapy generally describes the transfer of a desired nucleic acid sequence, located on a transport vector, directly into an individual in need of therapy. This gene therapy approach does not require that the target cells be first removed and manipulated *in vitro*. Once the vector containing the desired nucleotide sequence is introduced into the individual, the vector moves into the nucleus of the target cell and the nucleotide sequence of interest integrates into the chromosomal DNA of the target cell with varying degrees of efficiency. A number of well documented methods exist for introducing nucleic acids into an individual requiring therapy such as direct injection of

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DNA and the use of recombinant viral vectors (Gene Therapy, A Handbook for Physicians, Mary Ann Liebert, Inc., 1994).

The present invention provides a method of treating both Type I and Type II diabetics through a different gene therapy approach. A stable mammalian cell line is transformed by a nucleic acid vector such that it secretes a GLP-1(7-37)-based protein, as defined by SEQ ID NO 1, followed by implantation into an individual needing treatment. Once implanted, the GLP-1(7-37)-based protein, in conjunction with high serum glucose levels, causes pancreatic beta cells to produce insulin in non-insulin dependent diabetes mellitus (NIDDM) patients and delays gastric emptying in both NIDDM and insulin dependent diabetes mellitus IDDM patients.

Accordingly, one embodiment of this invention provides a method of treating Type I or Type II diabetes in a mammal in need thereof comprising implanting a cell line transformed with a vector comprising a promoter driving expression of a DNA sequence encoding a protein of SEQ ID NO 1

His-Xaa¹-Glu-Gly-Thr-Phe-Thr-Ser-Asp-Val-Ser-Ser-Tyr-
Leu-Xaa²-Gly-Gln-Ala-Ala-Xaa³-Xaa⁴-Phe-Ile-Ala-Trp-Leu-
Val-Lys-Gly-Arg-Xaa⁵ (SEQ ID NO 1)

wherein

Xaa¹ is Ala, Gly, Val, Thr, and Ile;
Xaa² is Glu, Gln, Ala, Thr, Ser, and Gly;
Xaa³ is Lys, and Arg;
Xaa⁴ is Glu, Gln, Ala, Thr, Ser, and Gly; and,
Xaa⁵ is Gly-OH or is absent;
into said mammal such that it is immunologically isolated from the mammal's immune system and secretes a protein of SEQ ID NO 1 into said patient.

Preferred proteins of SEQ ID NO 1 are those in which Xaa¹ is Ala, Xaa² is Glu, Xaa³ is Lys, Xaa⁴ is Glu, and Xaa⁵ is Gly-OH. More preferred are those in which Xaa¹ is Ala, Gly, Val, Thr, and Ile; Xaa² is Glu, Gln, Ala, Thr, Ser,

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and Gly; Xaa³ is Lys, and Arg; Xaa⁴ is Glu, Gln, Ala, Thr, Ser, and Gly; and, Xaa⁵ is Gly-OH or is absent. Another preferred group are those in which Xaa¹ is Val and Xaa³ is Lys. A further preferred group of proteins are those wherein

5 Xaa¹ is Ala or Val, Xaa² Glu, Xaa³ is Lys or Arg, Xaa⁴ is Glu, and Xaa⁵ Gly-OH or is absent. Yet another preferred group are those in which Xaa¹ is Ala, Xaa² Glu, Xaa³ is Lys, Xaa⁴ is Glu, and Xaa⁵ Gly-OH. Still another preferred group is when Xaa¹ is Val, Xaa² Glu, Xaa³ is Lys, Xaa⁴ is Glu, and

10 Xaa⁵ Gly-OH.

Nucleotide sequences encoding any one of the polypeptides of SEQ ID NO 1 may be prepared by a variety of means readily apparent to those skilled in the art. Wholly synthetic nucleotide sequences or semi-synthetic sequences

15 derived in part from a natural GLP-1 gene may be used. Owing to the natural degeneracy of the genetic code, the skilled artisan will recognize that a sizable yet definite number of nucleotide sequences may be constructed which encode the proteins of SEQ ID NO 1. A synthetic DNA sequence encoding a

20 GLP-1-based protein of SEQ ID NO 1 may be prepared by techniques well known in the art in substantial accordance with the teachings of Brown, *et al.* (1979) *Methods in Enzymology*, Academic Press, N.Y., Vol. 68, pgs. 109-151. The DNA sequence may be generated using conventional DNA

25 synthesizing apparatus such as an Applied Biosystems Model 380A or 380B DNA synthesizer (commercially available from Applied Biosystems, Foster City, California). Commercial services are also available for the construction of such nucleotide sequences based on the amino acid sequence.

30 In one preferred embodiment of the invention as exemplified herein, the coding sequence for a protein of SEQ ID NO 1 is the following:

5' - CAT GCT GAA GGG ACC TTT ACC AGT GAT GTA AGT TCT TAT TTG
 GAA GGC CAA GCT GCC AAG GAA TTC ATT GCT TGG CTG GTG AAA
 35 GGC CGA GGA - 3' (SEQ ID NO 2).

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This sequence encodes the following protein of SEQ ID NO 1:

H₂N- His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu
 Glu Gly Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys
 Gly Arg Gly -OH (SEQ ID NO 3).

5 In another preferred embodiment of the invention as exemplified herein, the coding sequence for a protein of SEQ ID NO 1 is the following:

5' - CAT GTT GAA GGG ACC TTT ACC AGT GAT GTA AGT TCT TAT TTG
 GAA GGC CAA GCT GCC AAG GAA TTC ATT GCT TGG CTG GTG AAA
 10 GGC CGA GGA - 3' (SEQ ID NO 4).

This sequence encodes the following protein of SEQ ID NO 1:

H₂N- His Val Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu
 Glu Gly Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys
 Gly Arg Gly -OH (SEQ ID NO 5).

15 Coding regions for SEQ ID NO 1 may be fused to a leader sequence which signals the cell to secrete a precursor peptide of SEQ ID NO 1 that is subsequently processed by the cell during the secretion process to a protein of SEQ ID NO 1. Many such leader sequences are known in the art. One well
 20 known and preferred leader sequence is the hybrid tissue plasminogen activator/protein C prepropeptide described in Berg et al. *Biochem. Biophys. Res. Commun.* 179: 1289-1296 (1991). Typically nucleotide sequences encoding precursor peptides of SEQ ID NO 1 are flanked by linker DNA to
 25 facilitate enzymatic ligation into expression vectors as is later exemplified herein.

Once a suitable coding sequence of SEQ ID NO 1 is constructed and optionally fused and flanked by an appropriate leader sequence and linker DNA, the construct is
 30 ligated into an expression vector which is then introduced into an appropriate cell line. Construction of suitable vectors containing the desired coding and control sequences may be constructed by standard ligation techniques. Isolated

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plasmids or nucleotide fragments are cleaved, tailored, and religated in the manner necessary to achieve the desired plasmids.

To effect the expression of a polypeptides of SEQ
5 ID NO 1, one ligates a nucleotide sequence encoding the
polypeptide into an appropriate recombinant nucleotide
expression vector through the use of appropriate enzymes.
The nucleotide sequence encoding a polypeptide of SEQ ID NO 1
is designed to possess restriction endonuclease cleavage
10 sites at either end of the DNA to facilitate isolation from
and integration into these amplification and expression
plasmids. The coding sequence may be readily modified by the
use of synthetic linkers to facilitate the incorporation of
the coding sequence into the desired cloning vectors by
15 techniques well known in the art. The particular
endonucleases employed will be dictated by the restriction
endonuclease cleavage pattern of the parent expression vector
to be employed. The choice of restriction sites are chosen
so as to properly orient the coding sequence such that it is
20 properly associated with the promoter and ribosome binding
site of the expression vector, both of which are functional
in the host cell in which a compound of SEQ ID NO 1 is to be
expressed.

In addition to the desired nucleotide sequence which
25 will code for the therapeutic protein, the expression vector
may contain several other functional elements. One such
element is the promoter and upstream regulatory sequences
which control the level of expression of the protein of
interest. Some expression vectors contain promoters and
30 regulatory sequences which normally regulate transcription of
cellular genes. One such promoter is the mouse
metallothionein-I promoter which has been shown to function
both *in-vitro* and *in-vivo* (Palmiter et al., *Nature* **300**: 611 -
615, 1982). In addition, promoters and regulatory sequences
35 from viruses are frequently used in expression vectors
(Dijkema et al., *EMBO J.* **4**, 471, 1985; Gorman et al., *Proc.*
Natl. Acad. Sci. **79**: 6777, 1982; Boshart, et al. *Cell* **41**:

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521, 1985). Although, Verma et al. have shown that the retrovirus promoter and enhancer sequences do not function for long periods of time in-vivo. In addition, the expression vector also carries an origin of replication as well as marker sequences which are capable of providing phenotypic selection in transformed cells.

Because the proteins useful in the present invention do not require post-translational processing mechanisms other than enzymatic removal of the propeptide leader sequence, many stable human cell lines are consistent with the practice of the invention. One preferred cell line is the human embryonal kidney cell line 293, available from the permanent collection of the American Type Culture Collection.

A number of well known methods exist for introducing the genetic material into target cells such as chemical (calcium phosphate precipitation), physical (electroporation and microinjection), and viral methods (adenovirus, retrovirus, and adeno-associated virus) (Methods for Gene Transfer, Gene Therapy, Mary Ann Liebert, Inc., 1994). All such methods are consistent with the practice of the present invention. The techniques of transforming mammalian cells with the aforementioned vector types are well known in the art and may be found in such general references as Maniatis, et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York or Current Protocols in Molecular Biology, Vol. 1, (1988), Wiley Interscience, and supplements.

Stable transformed cell lines that express proteins of SEQ ID NO 1 must then be implanted into the individual in need of such treatment. Because such transformed cell lines generally will be histologically incompatible with the individuals receiving them, the cells must to be protected from the recipient's immune system. One way of protecting the implanted cells is by masking them with F(ab')₂ fragments specific for HLA class I antigens. Immunological masking

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methods are well known in the art. For example, see Faust et al. *Science* 252:1700-1702 (1991). Other means for protecting the implanted cells from the recipient's immune system are consistent with this invention. Such methods include but are not limited to encapsulation in semi-permeable membranes (Lanza et al. *Diabetes* 41: 1503 - 1510) and through the use of immunosuppressants (Rynasiewicz et al., *Diabetes* 31: 92 - 108, 1982).

By way of illustration, the following examples are provided to help describe how to make and practice the various embodiments of the invention. These examples are in no way meant to limit the scope of the invention.

Example 1

Construction of Intermediate

Plasmid pLP53-tLB+GLP-1

A. Preparation of BglII-Mung Bean-AvrII Digested pLP53-tLB

The plasmid pLP53-tLB was isolated from *E. coli* K12 AG1 (on deposit under terms of the Budapest Treaty and made part of the permanent stock culture collection of the Northern Regional Research Laboratories (NRRL), agricultural Research Service, U.S. Dept. of Agriculture, Peoria, IL 61604 under accession number NRRL B-18714) using the Plasmid Purification Midi Kit. (Qiagen, Inc., 9600 DeSoto Avenue, Chatsworth, CA 91311).

Sixty μ l (approximately 20 μ g) of pLP53-tLB DNA was digested with 2 μ l (20 units) of BglII in a 70 μ l reaction volume containing 50mM Tris-HCl (pH 8.0), 10mM MgCl₂, and 100mM NaCl. The sample was incubated at 37°C for one hour. 17.5 μ l of 5x stop mix (25% glycerol, 2% SDS, 0.05% bromophenol blue, 0.05% xylene cyanol in water) was added and then the reaction was heated at 70°C for 15-20 minutes to inactivate the restriction enzyme. The mixture was spin dialyzed using G-50 Sephadex Quick Spin columns (Boehringer Mannheim Corporation, P.O. Box 50414, 9115 Hague Road,

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Indianapolis, IN 46250-0414) to remove the reaction components.

The 5' protruding ends created by cleavage with BglII were removed using Mung Bean Nuclease. The BglII digested pLP53-tLB DNA was incubated with 0.3 μ l (approximately 3.3 units) of Mung Bean Nuclease in a 100 μ l reaction volume containing 10mM Tris-HCl (pH 7.9 at 25°C), 10mM MgCl₂, 50mM NaCl, 1mM DTT, and 1mM ZnSO₄. The reaction was allowed to proceed for 30 minutes at 30°C. One μ l of 1% SDS was added to inactivate the nuclease. Due to an incomplete BglII digest, the digested and undigested DNA was separated by gel electrophoresis. Ten μ l of gel loading dye (0.25% bromophenol blue, 0.25% xylene cyanol, 30% glycerol in water) was added to the reaction. The reaction was loaded into the preparative well of a 1.5% NuSieve GTG agarose (FMC Bioproducts, 191 Thomaston Street, Rockland, ME 04841)/TAE buffer gel and then electrophoresed. The gel was stained with ethidium bromide and the DNA was visualized by ultraviolet light. The digested DNA band was excised with a scalpel and placed into two micro-tubes. The DNA was purified from the low melting point agarose using the Wizard PCR Preps DNA Purification System (Promega, 2800 Woods Hollow Road, Madison, WI 53711-5399).

One hundred μ l of BglII-Mung Bean digested pLP53-tLB DNA was further digested with 4 μ l (approximately 16 units) of AvrII in a reaction volume of 120 μ l containing 10mM Tris-HCl (pH 7.9 at 25°C), 10mM MgCl₂, 50mM NaCl, 1mM DTT. The sample was incubated at 37°C for 30 minutes. To prevent recircularization, the BglII-Mung Bean-AvrII digested pLP53-tLB DNA was dephosphorylated (removal of 5' phosphate groups) by the addition of 2 μ l (2 units) of calf intestinal alkaline phosphatase to the reaction. The sample was incubated at 37°C for an additional 30 minutes. Twenty-four μ l of 5x stop mix was added. The sample was heated at 70°C for 15-20 minutes to inactivate the enzymes and then spin dialyzed using G-50 Sephadex Quick Spin columns (Boehringer Mannheim Corporation, P.O. Box 50414, 9115 Hague Road,

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Indianapolis, IN 46250-0414) in order to remove the AvrII produced small DNA fragments. The DNA was precipitated by addition of 0.1 volume of 3M sodium acetate (pH 5.2) and 2.5 volumes of absolute ethanol. This mixture was mixed
5 thoroughly and then chilled to -20°C. The precipitate was collected by centrifugation for 30 minutes. The supernatant was discarded and the pellet was washed with 700 µl of cold 70% ethanol. The sample was centrifuged for 15 minutes. The supernatant was discarded, the DNA pellet was dried and then
10 resuspended in 25 µl of water.

B. Preparation of GLP-1 Linker

The following single stranded DNA segments were conventionally synthesized by methods well known in the art
15 on an automated DNA synthesizer (model 394 Applied Biosystems 850 Lincoln Center Drive, Foster City, CA 94404-1128) using β-cyanoethyl phosphoramidite chemistry.

GLP-1.1

20 5' - GACATGCTGA AGGGACCTTT ACCAGTGATG TAAGTTCTTA TTTGGAAGGC
CAAGCTGCCA AGGAATTCAT TGCTTGGCTG GTGAAAGGCC GAGGATAGGG
ATCCC - 3' (SEQ ID NO 6)

GLP-1.2

25 5' - CTAGGGGATC CCTATCCTCG GCCTTTCACC AGCCAAGCAA TGAATTCCTT
GGCAGCTTGG CTTTCAAAT AAGAACTTAC ATCACTGGTA AAGGTCCCTT
CAGCATGTC - 3' (SEQ ID NO 7)

GLP-1.1 and GLP-1.2 are complementary DNA
30 molecules. The synthetic DNA molecules were dissolved in water and stored at less than 0°C.

To anneal the DNA strands, approximately 92.7 pmoles each of GLP-1.1 and GLP-1.2 were mixed in 50mM Tris-HCl (pH 7.4) and 10mM MgCl₂ in a total volume of 80 µl and
35 boiled for 5 minutes. The mixture was slowly brought to room temperature and then transferred to 4°C overnight. This process allowed the two complementary strands to anneal and

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form the double stranded DNA linker known as GLP-1. The linker was stored at -20°C. In order to be able to ligate into the dephosphorylated BglII-Mung Bean-AvrII digested pLP53-tLB DNA segment, the GLP-1 linker must have 5' phosphate groups. The phosphate groups were added by the use of the enzyme T4 polynucleotide kinase. The kinase reaction contained 80 µl of the GLP-1 linker, 0.33µM ATP, 70mM Tris-HCl (pH 7.6), 10mM MgCl₂, 100mM KCl, 1mM β-mercaptoethanol and 37.2 µl (372 units) of T4 polynucleotide kinase. The reaction was incubated at 37°C for 30 minutes. Sixteen µl of 500mM EDTA was added to stop the reaction. The reaction was extracted once with a mixture of phenol:chloroform:isoamyl alcohol (25:24:1) followed by an extraction with chloroform:isoamyl alcohol (24:1). One hundred µl of the aqueous layer was spin dialyzed using G-50 Sephadex Quick Spin columns (Boehringer Mannheim) in order to remove the reaction components. The DNA was precipitated by addition of 0.1 volume of 3M sodium acetate (pH 5.2), 0.1 volume of 100mM MgCl₂ and 2.5 volumes of absolute ethanol. This mixture was mixed thoroughly and then chilled at -20°C. The precipitate was collected by centrifugation for 30 minutes. The supernatant was discarded and the pellet was washed with 700 µl of cold 70% ethanol. The sample was centrifuged for 15 minutes. The supernatant was discarded, the DNA pellet was dried and then resuspended in 10 µl of water.

C. Final Construction of pLP53-tLB+GLP-1

The DNA prepared in Example 1A was ligated with linker GLP-1. Two µl of DNA prepared in Example 1A and 4 µl of GLP-1 linker were ligated in a reaction that contained 2 µl (2 units) of T4 DNA ligase, 50mM Tris-HCl (pH 7.6), 10mM MgCl₂, 1mM ATP, 1mM DTT, and 50% (w/v) polyethylene glycol-8000 in a total volume of 10 µl. The mixture was incubated at 16°C for 16 hours. The ligation was used to transform *E. coli* K12 INVαF' cells as generally described below.

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D. Transformation Procedure

Frozen competent *E. coli* K12 INV α F' cells were obtained from Invitrogen (3985 B Sorrento Valley Boulevard, San Diego, CA 92121). Two μ l of 0.5M β -mercaptoethanol were
5 added to 50 μ l of thawed competent cells. About 1-2 μ l of the ligation reaction was mixed with the cells. The cell-DNA mixture was incubated on ice for 30 minutes, heat-shocked at 42°C for exactly 30 seconds and then chilled on ice for 2 minutes. The cell-DNA mixture was diluted into 450 μ l of SOC
10 media (2% tryptone, 0.05% yeast extract, 10mM NaCl, 2.5mM KCl, 10mM MgCl₂, 10mM MgSO₄, 20mM glucose in distilled water) and incubated at 37°C for one hour in a rotary shaker set at about 225 rpm. Aliquots of up to 200 μ l were plated on TY-agar plates (1% tryptone, 0.5% yeast extract, 1% NaCl, and
15 1.5% agar, pH 7.4) containing 100 μ g/ml ampicillin and then incubated at 37°C until colonies appear.

E. DNA Isolation

Following transformation, ampicillin resistant
20 cells were picked and inoculated into 3 ml of TY broth (1% tryptone, 0.5% yeast extract, 1% NaCl, pH 7.4) containing 100 μ g/ml ampicillin. These cultures were grown for about 16 hours at 37°C with aeration. Plasmid DNA was isolated from cultures using Wizard Minipreps obtained from Promega (2800
25 Woods Hollow Road, Madison, WI 53711-5399). Recombinant plasmids were identified by digestion with restriction endonucleases followed by gel electrophoresis analysis.

To obtain larger amounts of pLP53-tLB+GLP-1 plasmid DNA, large scale isolation was performed using the Plasmid
30 Purification Midi Kit (Qiagen, Inc.).

Example 2

Construction of pGT-h+tLB+GLP-1

A. Preparation of BclI Digested pGT-h

The plasmid pGT-h was isolated from *E. coli* K12 GM48
35 (on deposit under terms of the Budapest Treaty and made part

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of the permanent stock culture collection of the NRRL under accession number B-18592 using the Plasmid Purification Midi Kit (Qiagen, Inc.).

Ten μg (37.5 μl) of pGT-h DNA was digested to completion with 2 μl (20 units) of BclI in a 45 μl reaction volume containing 50mM Tris-HCl (pH 8.0), 10mM MgCl_2 , 50mM NaCl. The sample was incubated at 50°C for 1 hour. Eleven μl of 5x stop mix was added to the reaction mixture. The mixture was heated at 70°C for 15-20 minutes to inactivate the restriction enzyme and then spin dialyzed using G-50 Sephadex Quick Spin columns (Boehringer Mannheim) in order to remove the reaction components. The DNA was precipitated by adding 0.1 volume of 3M sodium acetate (pH 5.2) and 2.5 volumes of absolute ethanol. This mixture was mixed thoroughly and then chilled at -20°C. The precipitate was collected by centrifugation for 30 minutes. The supernatant was discarded and the pellet was washed with 700 μl of cold 70% ethanol. The sample was centrifuged for 15 minutes. The supernatant was discarded, the DNA pellet was dried and then resuspended in 20 μl of water.

Calf intestinal alkaline phosphatase was used to remove the 5' phosphate groups from the DNA segment in order to prevent recircularization of the pGT-h. Ten μl of the BclI digested pGT-h DNA was treated with 1 μl (1 unit) of calf intestinal alkaline phosphatase in a 15 μl reaction containing 50mM Tris-HCl (pH 8.5 at 20°C) and 0.1mM EDTA. The reaction was allowed to proceed for 45 minutes at 37°C. The phosphatase was inactivated by the addition of 1 μl of 500mM EDTA and then heating at 65°C for 10 minutes. The reaction volume was increased to 100 μl with water and then extracted twice with phenol:chloroform:isoamyl alcohol (25:24:1) followed by extraction with chloroform: isoamyl alcohol (24:1). The DNA was recovered from the aqueous layer by the addition of 0.1 volumes of 3M sodium acetate (pH 5.2) and 2.5 volumes of absolute ethanol. The mixture was mixed thoroughly and then chilled at -20°C. The precipitate was collected by centrifugation for 30 minutes. The supernatant

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was discarded and the pellet was washed with 700 μ l of cold 70% ethanol. The sample was centrifuged for 15 minutes. The supernatant was discarded, the DNA pellet was dried and then resuspended in 25 μ l of water.

5

B. Preparation of pLP53-tLB+GLP-1 BamHI Fragment

Thirty-five μ l (10.6 μ g) of pLP53-tLB+GLP-1 DNA, prepared in Example 1, was digested with 0.5 μ l (25 units) of BamHI in a 40 μ l reaction volume containing 50mM Tris-HCl (pH 8.0), 10mM MgCl₂, and 100mM NaCl. The reaction was allowed to proceed at 37°C for one hour. Five μ l of gel loading dye was added to the reaction. The reaction was loaded into the preparative well of a 4% NuSieve GTG agarose/TAE buffer gel. The DNA was electrophoresed for about one hour at 70 constant volts. The gel was stained with ethidium bromide and then the DNA was visualized by ultraviolet light. The desired 213 base pair DNA band was excised using a scalpel. The DNA was purified from the low melting point agarose using Wizard PCR preps (Promega).

20 C. Final Construction of pGT-h+tLB+GLP-1

The DNA prepared in Example 2A was ligated with DNA prepared in Example 2B. One μ l of DNA from Example 2A and 10.5 μ l of DNA from Example 2B were ligated in a reaction that contained 2 μ l (2 units) of T4 DNA ligase, 50mM Tris-HCl (pH 7.6), 10mM MgCl₂, 1mM ATP, 1mM DTT, and 50% (w/v) polyethylene glycol-8000 in a total volume of 20 μ l. The mixture was incubated at 16°C for 16 hours. The ligation reaction was used to transform *E. coli* K12 INV α F' as described in Example 1D. Plasmid DNA was isolated from ampicillin resistant cultures as described in Example 1E.

To obtain larger amounts of pGT-h+tLB+GLP-1 plasmid DNA for the purpose of transfection of mammalian cells, large scale isolation was performed using the alkaline lysis method.

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Example 3Construction of pGT-h+tLB+Val8GLP-1

The plasmid pGT-h+tLB+Val8GLP-1 was constructed substantially in accordance with Examples 1 and 2. To accommodate the change in the amino acid sequence (Ala to Val at Xaa¹ in SEQ ID NO 1) the following coding sequences were substituted for those described in Example 1B:

Val8GLP-1.1

10 5' - GACATGTTGA AGGGACCTTT ACCAGTGATG TAAGTTCTTA TTTGGAAGGC
CAAGCTGCCA AGGAATTCAT TGCTTGGCTG GTGAAAGGCC GAGGATAGGG
ATCCC - 3' (SEQ ID NO 8)

Val8GLP-1.2

15 5' - CTAGGGGATC CCTATCCTCG GCCTTTCACC AGCCAAGCAA TGAATTCCTT
GGCAGCTTGG CCTTCCAAAT AAGAACTTAC ATCACTGGTA AAGGTCCCTT
CAACATGTC - 3' (SEQ ID NO 9)

Example 4Construction of Intermediate

20 Plasmid pM100-neo

A. Preparation of EcoRI Digested pM100

The plasmid pM100 (pOK12) was isolated from *E. coli* K12 RR1ΔM15 using Magic Minipreps (Promega). See Vieira and Messing, Gene 100:189-94, 1991). Forty μl of pM100 DNA was
25 digested to completion with 3 μl of EcoRI in a reaction volume of 50 μl containing 50mM Tris-HCl (pH 8.0), 10mM MgCl₂, and 100mM NaCl. The sample was incubated at 37°C for 2 hours. The digested DNA was precipitated with ethanol. The final DNA pellet was resuspended in 30 μl of water.

30

B. Preparation of pBK-neo EcoRI Fragment

The plasmid pBK-neo 1 (described in U S Patent No: 5,550,036, herein incorporated by reference, and available from the American Type Culture Collection under terms of the

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Budapest Treaty via Accession No. Atcc 37224) was isolated from *E. coli* K12 HB-1 using the large scale alkaline lysis method. Three μ l (26.3 μ g) of pBK-neo DNA was digested to completion with 7 μ l (15 units) of *Eco*RI in a reaction volume of 200 μ l containing 50mM Tris-HCl (pH 8.0), 10mM MgCl₂, and 100mM NaCl. The sample was incubated at 37°C. Fifty μ l of the reaction was loaded into the preparative well of an agarose/TAE buffer gel and then electrophoresed. The desired 4.2 Kb DNA band was isolated from the agarose by electrophoresing onto DEAE-cellulose membrane. Following elution from the DEAE-cellulose membrane, the DNA was precipitated with ethanol. The final DNA pellet was resuspended in 30 μ l of water.

15 C. Final Construction of pM100-neo

The DNA prepared in Example 4A was ligated with DNA prepared in Example 4B. Two μ l of DNA from Example 4A and 2 μ l of DNA from Example 4B were ligated in a reaction that contained 1 μ l (1 unit) of T4 DNA ligase, 50mM Tris-HCl (pH 7.6), 10mM MgCl₂, 1mM ATP, 1mM DTT, and 50% (w/v) polyethylene glycol-8000 in a total volume of 16 μ l. The mixture was incubated at 16°C for 16 hours. Ten μ l of the ligation reaction was used to transform *E. coli* K12 RR1 Δ M15 as described in Example 5D. Aliquots of up to 200 μ l were plated on TY-agar plates (1% tryptone, 0.5% yeast extract, 1% NaCl, and 1.5% agar, pH 7.4) containing kanamycin and then incubated at 37°C until colonies appear.

D. DNA Isolation

Following transformation, kanamycin resistant cells were picked and inoculated into 5 ml of TY broth (1% tryptone, 0.5% yeast extract, 1% NaCl, pH 7.4) containing kanamycin. These cultures were grown for about 8 hours at 37°C with aeration. Plasmid DNA was isolated from cultures using Magic Minipreps obtained from (Promega). Recombinant plasmids were identified by digestion with restriction endonucleases followed by gel electrophoresis analysis.

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To obtain larger amounts of pM100-neo plasmid DNA, large scale isolation was performed using the Plasmid Purification Kit (Qiagen, Inc.).

Example 5

5 Construction of pMT-h+tLB+Val8GLP-1

A. Preparation of Bst1107I-BclI Digested pGT-h

The plasmid pGT-h was isolated as described in substantial accordance with Example 2A. Three µg (4.6 µl) of pGT-h DNA was digested to completion with 1 µl (8 units) of
10 Bst1107I in a 10 µl reaction volume containing 10mM Tris-HCl, 10mM MgCl₂, 100mM KCl (pH 8.5 at 37°C). The sample was incubated at 37°C for 1 hour. The Bst1107I digested pGT-h DNA was purified from the reaction components using the Wizard DNA Clean-Up System (Promega). The Bst1107I digested
15 pGT-h DNA was concentrated in a 6.7 µl volume using a microcon 50 (Amicon, Inc. 72 Cherry Hill Drive, Beverly, MA 01915).

The 6.7 µl of Bst1107I digested pGT-h DNA was further digested with 1 µl (10 units) of BclI in a reaction
20 volume of 10 µl containing 50mM Tris-HCl (pH 8.0), 10mM MgCl₂, 50mM NaCl. The sample was incubated at 50°C for 1 hour. To prevent any possible recircularization, the Bst1107I-BclI digested pGT-h was dephosphorylated (removal of
25 5' phosphate groups) by the addition of 1 µl (1 unit) of calf intestinal phosphatase to the sample. The sample was incubated at 37°C for 30 minutes. Gel loading dye (0.25% bromophenol blue, 0.25% xylene cyanol, 30% glycerol in water) was added to the reaction. The reaction was loaded into the preparative well of a 1% SeaPlaque GTG agarose/TAE buffer gel
30 and then electrophoresed. The gel was stained with ethidium bromide and then the DNA was visualized by ultraviolet light. The desired 6.2 Kb DNA band was excised with a scalpel and placed into a micro-tube. The DNA was purified from the low melting point agarose using the Wizard PCR Preps DNA
35 Purification System (Promega).

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B. Preparation of pM100-neo EcoRV-BglII Fragment

Five µg (3.8 µl) of pM100-neo DNA constructed in Example 4 was digested to completion with 1 µl (10 units) of
5 EcoRV in a 10 µl reaction volume containing 50mM Tris-HCl (pH 8.0), 10mM MgCl₂, 50mM NaCl. The reaction was incubated at 37°C for 1 hour. The EcoRV digested pM100-neo was further digested with 1 µl (10units) of BglII in a 20 µl reaction volume containing 50mM Tris-HCl (pH 8.0), 10mM MgCl₂, 50mM
10 NaCl. The sample was incubated at 37°C for 1 hour. Gel loading dye (0.25% bromophenol blue, 0.25% xylene cyanol, 30% glycerol in water) was added to the reaction. The reaction was loaded into the preparative well of a 1% SeaPlaque GTG agarose/TAE buffer gel and then electrophoresed. The gel was
15 stained with ethidium bromide and then the DNA was visualized by ultraviolet light. The desired 1.8 Kb DNA band was excised with a scalpel and placed into a micro-tube. The DNA was purified from the low melting point agarose using the Wizard PCR Preps DNA Purification System (Promega).

20

C. Final Construction of pMT-h+tLB+Val8GLP-1

The DNA prepared in Example 5A was ligated with the DNA prepared in Example 5B and the DNA prepared in Example 3 (pLP53-tLB+Val8GLP-1 BamHI fragment). Four µl of DNA from
25 Example 5A, 3 µl of DNA from Example 5B and 12 µl of DNA prepared in Example 3 (pLP53-tLB+Val8GLP-1 BamHI fragment) were ligated in a reaction that contained 1 µl (1 unit) of T4 DNA ligase, 50mM Tris-HCl (pH 7.6), 10mM MgCl₂, 1mM ATP, 1mM DTT, and 50% (w/v) polyethylene glycol-8000 in a total volume
30 of 25 µl. The mixture was incubated at 16°C for 16 hours.

Frozen competent E.coli K12 DH5α cells were transformed using about 3-4 µl of the ligation reaction in substantial accordance with Example 1D, and the plasmid DNA was isolated in substantial accordance with Example 1E.

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Example 6Construction of Stable Cell lines

Plasmid DNA, either pGT-h+tlb+GLP-1, pGT-h+tlb+val8GLP-1, or pMT-h+tlb+val8GLP-1 was transfected into
5 human embryonic kidney 293 cells using the stable CaPO₄ method
contained in the Mammalian Transfection Kit available from
Stratagene (11011 North Torrey Pines Road, LaJolla, CA
92037). Selection was achieved by the addition of 300µg/ml
of hygromycin B (Eli Lilly and Company Indianapolis, IN
10 46285) to the culture medium. Monoclonal cell lines were
expanded and screened for the ability to secrete the
corresponding protein of SEQ ID NO 1 into the culture medium.
The presence of biologically active GLP-1(7-37)-based protein
in the culture medium was determined by measuring the amount
15 of luciferase enzyme present in a biological system that
expressed luciferase enzyme following stimulation with GLP-1.

Example 7Implantation

The transformed 293 cell were cultured then
20 surgically transplanted under the kidney capsule of 8 week
old Zucker Diabetic Fatty (ZDF/GmiTM-fa/fa) male rats. Under
isofurane anesthesia, a dorsal incision was made just
posterior to the diaphragm, and using a rib spreader, the
kidney was exposed. Approximately 20 million transformed 293
25 cells, in 200 µl of Hank's buffer, were injected just under
the kidney capsule using a 23 gauge blunt needle. The
incision was sutured and protected from chewing with wound
clips.

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We Claim:

1. A method of treating Type I or Type II diabetes in a mammal in need thereof comprising implanting a cell line transformed with a vector comprising a promotor driving expression of a DNA sequence encoding a protein of the formula:

His-Xaa¹-Glu-Gly-Thr-Phe-Thr-Ser-Asp-Val-Ser-Ser-Tyr-
Leu-Xaa²-Gly-Gln-Ala-Ala-Xaa³-Xaa⁴-Phe-Ile-Ala-Trp-Leu-
Val-Lys-Gly-Arg-Xaa⁵ (SEQ ID NO 1)

10 wherein

- Xaa¹ is Ala, Gly, Val, Thr, and Ile;
Xaa² is Glu, Gln, Ala, Thr, Ser, and Gly;
Xaa³ is Lys, and Arg;
Xaa⁴ is Glu, Gln, Ala, Thr, Ser, and Gly; and,
15 Xaa⁵ is Gly-OH or is absent;
into said mammal such that it is immunologically isolated from the mammal's immune system and secretes a protein of SEQ ID NO. 1 into said patient.

- 20 2. A method of treating Type I or Type II diabetes in a mammal in need thereof comprising implanting a cell line transformed with a vector comprising a promotor driving expression of a DNA sequence encoding a protein of SEQ ID NO 1 into said mammal wherein said mammal is under
25 immunosuppression therapy.

3. The method of Claims 1 or 2 wherein Xaa¹ is Ala or Val, Xaa² Glu, Xaa³ is Lys or Arg, Xaa⁴ is Glu, and Xaa⁵ Gly-OH or is absent.

30

4. The method of Claims 1 or 2 wherein Xaa¹ is Ala, Xaa² Glu, Xaa³ is Lys, Xaa⁴ is Glu, and Xaa⁵ Gly-OH.

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5. The method of Claims 1 or 2 wherein Xaa¹ is Val, Xaa² Glu, Xaa³ is Lys, Xaa⁴ is Glu, and Xaa⁵ Gly-OH.

5 6. The method of Claims 1 or 2 wherein the promotor is a viral promotor.

7. The method of Claims 1 or 2 wherein the promotor is a metallothionein promotor.

10

8. The method of Claims 1 or 2 wherein the DNA coding sequence is

5' - CAT GCT GAA GGG ACC TTT ACC AGT GAT GTA AGT TCT TAT TTG
GAA GGC CAA GCT GCC AAG GAA TTC ATT GCT TGG CTG GTG AAA
15 GGC CGA GGA - 3'. (SEQ ID NO 2)

9. The method of Claims 1 or 2 wherein the DNA coding sequence is

5' - CAT GTT GAA GGG ACC TTT ACC AGT GAT GTA AGT TCT TAT TTG
20 GAA GGC CAA GCT GCC AAG GAA TTC ATT GCT TGG CTG GTG AAA
GGC CGA GGA - 3'. (SEQ ID NO 4)

10. The method of Claims 1 or 2 wherein the cell line is the human embryonal kidney cell line 293 transformed
25 with a vector selected from the group consisting of pGT-h+tLB+GLP-1, pGT-h+tLB+Val8GLP-1, or pMT-h+tLB+Val8GLP-1.

11. The method of Claims 1 or 2 wherein the cell line is the human embryonal kidney cell line 293 transformed
30 with the vector pGT-h+tLB+GLP-1.

12. The method of Claims 1 or 2 wherein the cell line is the human embryonal kidney cell line 293 transformed with the vector pGT-h+tLB+Val8GLP-1.

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13. A method of treating Type I or Type II diabetes in a mammal in need thereof comprising injecting an expression vector of any one of Claims 1 to 12 directly into the mammal such that the expression vector is incorporated into a cell of the mammal and secretes a protein of SEQ ID NO. 1.

14. A stable transformed cell line of any one of Claims 1 to 12.

15. A vector of any one of Claims 1 to 12.

16. A method of treating Type I or Type II diabetes in a mammal in need thereof comprising implanting a cell line transformed with a vector comprising a promotor driving expression of a DNA sequence encoding a protein of the formula:

His-Xaa¹-Glu-Gly-Thr-Phe-Thr-Ser-Asp-Val-Ser-Ser-Tyr-
Leu-Xaa²-Gly-Gln-Ala-Ala-Xaa³-Xaa⁴-Phe-Ile-Ala-Trp-Leu-
Val-Lys-Gly-Arg-Xaa⁵ (SEQ ID NO 1)

wherein

Xaa¹ is Ala, Gly, Val, Thr, and Ile;
Xaa² is Glu, Gln, Ala, Thr, Ser, and Gly;
Xaa³ is Lys, and Arg;
Xaa⁴ is Glu, Gln, Ala, Thr, Ser, and Gly; and,
Xaa⁵ is Gly-OH or is absent;

into said mammal such that it is immunologically isolated from the mammal's immune system substantially as hereinbefore described with reference to any one of the Examples.

17. A vector encoding a protein of SEQ ID NO 1 substantially as hereinbefore described with reference to any one of the Examples.

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18. A stable mammalian cell line transformed with a vector capable of secreting a protein of SEQ ID NO 1 substantially as hereinbefore described with reference to any one of the Examples.

5

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US97/01978

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : C12N 5/00, 15/00, 15/16, 15/09; A61K 48/00

US CL : 424/93.1; 435/172.3, 320.1, 69.1; 514/44; 935/62, 70, 34, 65

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 424/93.1; 435/172.3, 320.1, 69.1; 514/44; 935/62, 70, 34, 65

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

STN, APS, MEDLINE, CAPLUS, BIOSIS, EMBASE

search terms: gene therapy, ex vivo, glucagon like peptide, glp, transfection, transduction

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	STEWART et al. Insulin Delivery by Somatic Cell Gene Therapy. Journal of Molecular Endocrinology. December 1993, Vol. 11, No. 3, pages 335-341.	1-12, 16-18
Y, P	YAJIMA et al. Construction and Characterization of a Recombinant Adenovirus Vector Carrying the Human Preproinsulin Gene Under the Control of the Metallothionein Gene promoter. Biochemical and Biophysical Research Communications, 1996, Vol. 229, No. 3, pages 778-787.	1-12, 16-18
Y, P	LEECH et al. Signal Transduction of PACAP and GLP-1 in Pancreatic Beta Cells. Annals of the New York Academy of Sciences. 26 December 1996, Vol. 805, pages 81-92.	1-12, 16-18

☒ Further documents are listed in the continuation of Box C.
 ☐ See patent family annex.

* Special categories of cited documents:	*T	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X*	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	*Y*	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*Z*	document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means		
P document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search 14 MAY 1997	Date of mailing of the international search report 11 JUL 1997
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230	Authorized officer. KAREN M. HAUDA Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US97/01978

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	THORENS et al. Glucagon-like Peptide-I and the Control of Insulin Secretion in the Normal State and in NIDDM. Diabetes. September 1993, Vol. 42, No. 9, pages 1219-1225.	1-12, 16-18
Y	THORENS et al. Cloning and Functional Expression of the Human Islet GLP-1 Receptor. Diabetes. November 1993, Vol. 42, No. 11, pages 1678-1682.	1-12, 16-18
Y	GROMADA et al. Stimulation of Cloned Human Glucagon-Like Peptide 1 Receptor Expressed in HEK 293 Cells Induces cAMP-dependent Activation of Calcium-induced Calcium Release. FEBS Letters. 09 October 1995, Vol. 373, No. 2, pages 182-186.	1-12, 16-18
Y	STEWART et al. Insulin-releasing Pituitary Cells as a Model for Somatic Cell Gene Therapy in Diabetes Mellitus. Journal of Endocrinology. August 1994, Vol. 142, No. 2, pages 339-343.	1-12, 16-18
Y	THORENS. Glucagon-like Peptide-1 and Control of Insulin Secretion. Diabete Et Metabolisme. December 1995, Vol. 21, No. 5, pages 311-318.	1-12, 16-18
Y	FEHMANN et al. Ligand-specificity of the Rat GLP-I Receptor Recombinantly Expressed in Chinese Hamster Ovary (CHO-) Cells. Zeitschrift Fur Gastroenterologie. April 1994, Vol. 32, No. 4, pages 203-207.	1-12, 16-18
Y, P	WO 96/25487 A1 (ECOLE POLYTECHNIQUE FEDERALE DE LAUSANNE) 22 August 1996 (22.08.96), see entire patent.	1-12, 16-18
Y	US 5,399,346 A (ANDERSON et al.) 21 March 1995 (21.03.95), see entire patent.	1-12, 16-18

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US97/01978

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: 1-18
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

Claims 1-18 contain amino acid sequences. A sequence disk was not submitted with this application, so these claims could not be properly searched. However, Claims 1-18 were searched on the recited claims and the invention as presented in the description as was possible based on the text of the claims.

3. ☒ Claims Nos.: 13-15
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.